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Spatio-temporal model of avian influenza spread risk

Iglesias, I[a*]; Sánchez-Vizcaíno JM[b]; Muñoz[a], M.J; Martínez, M[a,b]; de la Torre A.[a]

[a] *Epidemiology & Environmental Health Department, Animal Health Research Center (CISA-INIA), 28130 Madrid, Spain*

[b] *Animal Health Department, Complutense University of Madrid,28040 Madrid, Spain*

** Corresponding author: Irene Iglesias Martín; Telephone: 0034 91 6202300; e-mail:iglesias@inia.es*

Abstract: HPAI virus has caused significant economic losses in the poultry industry. Backyard and outdoor poultry farms (BOPF) can play an important role in the spread of the disease. A spatio-temporal model has been developed to identify areas and periods at higher risk of HPAI spread in BOPF and applied on a Spanish region. Six risk factors were considered: Census, density, biosecurity, species susceptibility, proximity to risk wetlands and virus survival. A risk map was generated adding each risk factor as a spatial layer and a spatial-temporal analysis was conducted using scan statistics. Six clusters of spread risk of HPAI were identified in December and January. Despite the simplicity of the model, this system allows to focus the surveillance efforts in the highest risk areas and species. Thereby it could improve the efficiency of surveillance and control systems in terms of cost/benefit ratio

Keywords: spatial analysis; avian influenza; risk factors; modelling diseases; multicriteria decision, scan statistics.

1 Introduction: Highly pathogenic avian influenza (HPAI) virus strains have devastating consequences for poultry flocks because of their high transmissibility and high mortality rates. In the last years the high spread of the disease has caused significant economic losses in the poultry industry.

Surveillance may be defined as an active and systematic process for early detection and has been recognised by the Chief Veterinary Officers (CVOs) as one of the key elements of any animal health policy [1]. A critical component of any surveillance system is the cost of the sampling scheme in which disease detection is based. OIE has issued recommendations in Terrestrial Animal Health Code [2] and the European Commission has adopted [3] a surveillance risk-based approach by targeting the collection of samples to areas at higher risk. This type of surveillance strategy is particularly useful in backyard farms whose sampling is resource intensive because there are usually dispersed in small farms with small population (fewer than 100 heads).

Backyard and outdoor poultry farms (BORF) have played an important role in HPAI spreading in Asia [4] but information about Europe is controversial. HPAI epidemic in Italy (1999-2000) showed the importance of BORF in the disease spreading [5] while a marginal role was described in the Holland HPAI outbreaks [6]. It could be explained by a small size population (less likelihood of infected animals) and a marginal trade with the poultry industry. However, due to the low

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biosecurity and that their contact with wildbirds is more likely, this type of poultry farms could be act as a bridge between wild birds and domestic poultry industry, highlighting the importance of applying surveillance in BORF [7].

Spanish poultry production is ranked third in Europe, and represents an important percentage of the livestock economy in the country. Therefore, the spread of HPAI could have a high impact on poultry health and national economy. Only two occasional outbreaks (in 2006 and 2009) have been reported in Spain, both were directly or indirectly associated to wild birds [8] showing that the spreading risk by BORF (4% of poultry in Spain) is a priority. Moreover, introduction of HPAI by migratory birds has been identified as a relevant route in Spain due to this country hosts a large number of migratory birds susceptible to HPAI coming from countries with high infection probability [9].

Spatial analysis is the solution proposed in this paper for the application of risk assessment to identified spread risk areas of HPAI in BORF (about which available information is poor) for carrying out of surveillance in a targeted and resource efficient way. The study was carried out in Castilla León (CL), which is an autonomous region of Spain, third largest producer in poultry in Spain, including 2,538 backyards farms. This region has been considered on previous studies as a high risk area for the introduction of HPAI via wildlife birds and live poultry trade [9, 10].

Spatial analysis models allow the identification of risk zones and periods, making surveillance plans more effective and economical. Multicriteria Decision (MCD) combined with spatial analysis has been applied on the study of different zoonotic diseases such as Rift Valley Fever, tuberculosis and HPAI [11, 12, 13]. Other spatial tools such as the models of time-space scan statistic [14] were used to identify time-space clusters of diseases and have been applied to in many livestock diseases [12] such as HPAI H5N1 in domestic poultry and wild birds in Europe [15, 16].The aim of this study is to identify which areas present a higher risk of the spread of HPAI in BORF in CL using the combination of MCD and time-space scan statistic analysis. The methodology adopted could be extrapolated to other frameworks in the same country or in others. The results obtained would contribute to the improved surveillance and control plans against for HPAI in BORF.

2 Materials and methods: The spatio-temporal model of HPAI spread risk was developed in two consecutive steps. Firstly, a spatial deterministic model was constructed using a MCD method to identify risk areas of spread of HPAI. It was based on different risk factors regarding to farms characteristics and environmental parameters. Secondly, a spatio-temporal analysis was conducted to identify the period and locations at higher risk.

2.1.Data sources: "Location" (x,y) and "census" data from each of the 2,538 BORP (poultry, ducks, turkey, ostrich, quail, partridges, pigeons and pheasants) registered in CL were obtained from Regional government of CL; "Biosecurity" data were estimated from expert opinion and "Specie susceptibility" was extrapolated from scientific reports. Environmental characteristics, location and surface of wetlands were recorded from Spanish Birdlife (SEO), CORINE [17] and Spanish Ministry of Environmental. Monthly mean temperatures (2001-2007) were obtained from Meteorologycal Agency (AEmet).

2.2. Model: 6 risk factors were considered to evaluate the risk of each farm. Farm intrinsic factors were: Census "C", Density "D", Biosecurity "B" and species Susceptibility "S". "C" and "D" were estimated applying a surface Kernel model using Arc.Gis 9.3. (ESRI ©). "B" and "S" were ranked as showed in Table 1.

The extrinsic or environmental spread risk factors included in the model were the proximity of farms to risk wetlands ("Rw") and the survival of virus based on monthly temperature data ("Sm"). "Rw" was identified applying a logistic regression model which identify the risk of a wetland associated to wild birds HPAI outbreaks occurrence based on its environmental characteristics (salinity, waterbirds and the land use forestry) [18]. "Sm" was evaluated extrapolating temperatures data into survival times ("Sm") by using a HPAI virus survival curve ($y=-7.82\ln(x)+29.94$; $R^2=0.97$) based on bibliographical data obtained from EFSA [19].

All risk factors were normalized and added to each farm as a variable (D, C, B, S, Rw, Sm), for their inclusion in the model. Risk factors were analyzed as spatial layers (ArcGis9.3.) and integrated using the following equation $RT_{im}=[Rw*Sm]+[D*C*B*S]$; Where Rt_{im} is the risk of spread for each month (m) in each farm (i). Inverse distance weighting (IDW) [20] was used to create isopleth maps of the risk of spread of HPAI of each month in CL.

2.3.Time-spatial statistic: The normal model of the time-space scan statistic [14] was used to identify time-space clusters of risk of spread in CL. The null-hypothesis was that the risk is randomly distributed throughout the area and period of time under study. Failure to reject the null-hypothesis would be compatible with the application of a random surveillance in the farms throughout the region. Conversely, if intrinsic and extrinsic factors are positively clustering then the probability of risk of spread will be aggregated in those periods of times and regions in which those variables and forces are present. For cluster identification software builds cylinders and analyzes the significance of risk values inside and outsider. The base and the height of the cylinders represented, respectively, the spatial and temporal dimensions of the data. A Monte Carlo process implemented through a large number of simulations (n=999) was used to test the significance ($P<0.05$) of candidate clusters, i.e., the confidence that one has in that the candidate cluster represented a true cluster of risk of spread.

2.4. Sensitivity analysis: The identification of critical risk factors was made by a sensitivity analysis using Monte Carlo simulation (@Risk 5.5.© software). The resulting regression coefficients showed the relative influence of the each risk factor in the model**.**

3. Results: *3.1. Monthly model:* Areas that showed a highest and constant risk were located in 3 provinces: center of Segovia, southern Avila and East center of Leon (Figure 1a). December, January and February were the months that showed the maximum values of risk and July and August recorded the minimum values.

3.2. Time-spatial statistic: 6 significant time–space clusters of risk of spread of HPAI were identified in CL (Figure 1b). The area included in the main cluster showed an annual risk mean value higher than the annual maximum values of 66% of the regions studied. The cluster radios ranged from 4.87 to 37.51 km (average value=12.30 km) and comprised a surface between 74 and 4,421 km^2 with an average of 893 km^2.The number of farms included in each cluster varied between 24 and 842. Chicken was the majority specie in all of them over 92% (Table 2).The most significant clusters (1 and 2) had a higher diversity of species (Table 2).

3.3. Sensitivity analysis showed that "C" and "Rw" were the most influential risk factors in the model with 0.65 and 0.54 regression coefficients respectively. The risk factors "Sm", "D", "S" and "B" had a 0.27, 0.09, 0.02 and 0.02 regression coefficients respectively.

Discussion: The poultry sector is very important in Spanish livestock and so the heavy impact that the spread of HPAI could have on health and economy in Spain. According with the EU legislation is recommended to applied risk based surveillance such as method for the carrying out of surveillance for avian influenza in a targeted and resource efficient way. This paper propose using spatial analysis as solution for developing risk based surveillance in BORF which represents fewest percentages of total census of poultry in countries as Spain, but which could have been certain role in the spread of the disease in Europe [7].

The study here identified 6 time-space clusters in which risk of spread of HPAI was higher than that expected by chance. The two main clusters were: Cluster 1) in center of Segovia's province. This area has been identified as the highest risk area in all months especially in December. It should be highlight that the mean value of risk in each month in Segovia's province presented higher values than the maximum monthly risk in the provinces of Burgos, Palencia, Salamanca, Soria, Valladolid and Zamora. Cluster 2) South Avila's province is the second area of highest risk. This is an area classified as high risk throughout the year, specially between November and March, with a peak in December. It's significative that both areas showed low temperatures, presence of risk wetlands, high density of farms, low biosecurity in its farms and high susceptibility species (such as ducks and geese). These results suggest that in a hypothetical situation in case of shortages of resources these two areas and periods should be prioritized.

The agreement of results from the monthly IDW values and cluster analysis supports the conclusion that more spread risk exist during the coldest months. All clusters occurred between December and January showed the high time dependence of model derivate of the survival virus in the environmental, which is a significant risk factor as suggest Stallknecht et al [21].

The census of farms ("C") and the proximity of risk wetlands ("Rw") were identified as the most influential factors in spread of HPAI in BORF. The significance of "C" as risk factor are consistent with studies elaborated in the HPAI Italian epidemic [22]. Proximity of risk wetlands increases the probability of contact to wild bird which is determined as a main risk factor by EFSA [19]. Density ("D") showed lower weight in the model although it is a known risk factor for the spread of infective diseases. This result can be explained because BORF were usually dispersed and are not high influenced by commercial ruts as the industrial poultry.

Conclusions: Spread risk model developed is a tool easy to use and useful for veterinary health services as it allows identifying areas and periods of greatest risk for the spread of HPAI in BORF. Interestingly, despite the simplicity of the model, the system can be easily adjusted focusing surveillance efforts just in those higher risk areas and would help to reduce costs efforts. The study presented here is innovative and let's generate information so far not available which is designed to improve animal health and economic efforts in the fight against this disease. The methodology adopted can be extrapolated to other frameworks and the developed model can be updated continuously according with the policy and structural changes in the sector, to provide current information for answers according with the reality of a country at all times.

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Nomenclature

HPAI	High Pathogenic Avian Influenza	"B": Biosecurity	"Rw": Proximity of farms to risk wetlands
BORP	Backyard and Outdoor Poultry Farm	"C": Census of farm	
CL	Castilla Leon (Spanish region)	"S": Susceptivility	"Sm":Survival of virus based on

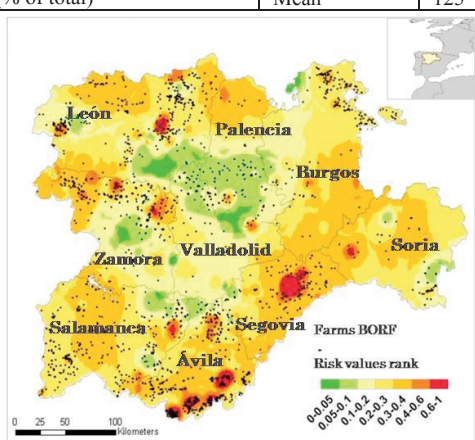
MCD	Multicriteria Decision	"D": Density	temperature data

Table 1 The values of the parameters Biosecurity and Susceptibility used in the model.

Parameter description	Level	Value	References	Normalization
Biosecurity	Backyard farms	1 (Low)	Expert opinion	1
	Semi-industrial outdoor	0.66 (Medium)		0.66
	Semi-industrial indoor	0.33 (High)		0.33
Susceptibility of species (This categorization assumed (comprised) the ability of each species to shed viruses and the probability of undetected disease)	Duck and goose: Potential asintomátic host shedding virus Susceptible to infection with all AI virus strains, but only some HP viruses produce clinical disease Quail: Require higher levels of testing than for chickens to detect infection . Could play a important role in HPAI spread	4 (High)	Cardona et al 2008 Ausvetplan, 2008 (Pérez et al., 2003a; Xu et al., 2007).	1
	Chicken and turkey. Phaisan Partridge	3 (Médium)	Perkins&Swayne, 2001	0.75
	Ostriche	2 (Low)	(Ausvetplan, 2008)	0.5
	Pigeon	1(Very low)	(Swayne, 2007),	0.25

Table 2. Significant clusters of spread risk of HPAI identified in CL by use or normal model of a time-space scan statistics. in a period of 5 yerarThe values of the parameters Biosecurity and Susceptibility used in the model.The radius, surface, period of time, farms inside, the spread risk inside and outside and the significance of each cluster are indicated in the 7 first rows. A classification of farms inside of clusters about species, production system and census are indicated in number and percentaje in the rest of table.

		Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Radius (Km)		12.14	37.51	4.87	5.08	7.78	6.42
Surface of cluester		463	2343	74	81	190	129
Period		December	December	January	December	January	December
Total nº of farms inside cluster		269	842	44	64	24	66
Mean value of risk inside cluster		0.945	0.665	0.626	0.522	0.598	0.501
Mean value of risk outside cluster		0.336	0.334	0.339	0.339	0.339	0.339
P value		0.001	0.001	0.001	0.004	0.01	0.021
Species: Nº farms (% of total)	Duck	3 (1.11)	6 (0.68)				
	Turkey	5 (1.85)	6 (0.68)				
	Chicken	257 (95.18)	848(96.58)	42 (97.67)	63 (100)	83 (92.22)	62 (92.53)
	Goose	1 (0.37)	5 (0.56)				
	Phaisan	1 (0.37)	5 (0.56)			1 (1.11)	
	Partridge	3 (1.11)	4 (0.45)	1 (2.32)		2 (2.22)	3 (4.47)
	Pigeon		4 (0.45)			2 (2.22)	1 (1.49)
	Ostrich		1 (0.11)			1 (1.11)	1 (1.49)
	Quail					1 (1.11)	()
Production system : Nº farms (% of total)	Indoor	255(94.444)	279(31.77)	1 (2.32)	56 (88.88)	65 (72.22)	15 (22.38)
	Semi-outdoor	16 (5.92)	390(44.42)	12 (27.9)	9 (14.28)	23 (25.55)	51(76.116)
	Outdoor		208(23.69)	31 (72.09)		1 (1.11)	1 (1.49)
Farm census: Nº farms (% of total)	Sume	33.675	10.958	5.304	716	35.455	4.939
	Mean	125	12	123	11	394	74



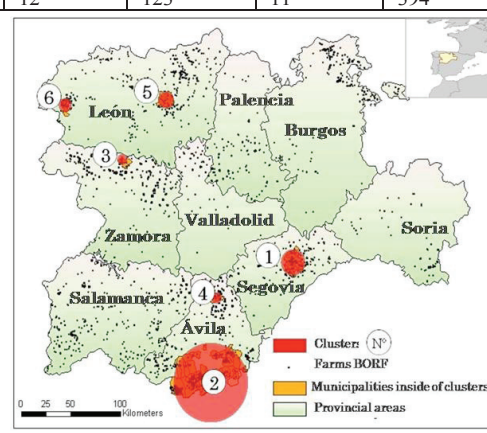


Fig. 1. (a) Risk of spread of HPAI in CL on January estimated using a MCD spatial method and represented using IDW.(b) Significant clusters (red circles) of spread risk of HPAI in CL detected by use of the normal model of the time-space scan statistics. The numbers refer to the designation of cluster presented in Table 2.

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